

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANTS: Chatterjee, Deb K.  
Solus, Joseph  
Yang, Shuwei

(ii) TITLE OF INVENTION: Polymerases for Analyzing or Typing Polymorphic  
Nucleic Acid Fragments and Uses Thereof

(iii) NUMBER OF SEQUENCES: 93

## (iv) CORRESPONDENCE ADDRESS:

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(C) CITY: Washington  
(D) STATE: DC  
(E) COUNTRY: USA  
(F) ZIP: 20005-3934

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: (To be assigned)  
(B) FILING DATE: 06-FEB-1998  
(C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: (To be assigned)  
(B) FILING DATE: 06-JAN-1998  
(C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/037,393  
(B) FILING DATE: 07-FEB-1997  
(C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Esmond, Robert W.  
(B) REGISTRATION NUMBER: 32,893  
(C) REFERENCE/DOCKET NUMBER: 0942.4250002

## (ix) TELECOMMUNICATION INFORMATION:

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## (2) INFORMATION FOR SEQ ID NO:1:

09891332-052701  
T04290-2E16860

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- (ii) MOLECULE TYPE: cDNA

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	CTGATGTCGT TTTCCTCACC ACTTTTTGGT TTCAGCTTTG CGGATGTTCC GGTAGACAAG	1380
	GCTGCGAACT ACTCCTGCGA GGATGCAGAC ATCACTTATA GGCTCTACAA GATACTCAGC	1440
	ATGAAGCTCC ATGAAGCGGA ACTTGAGAAC GTCTTCTACA GGATAGAGAT GCCGTTGGTG	1500
	AACGTTCTTG CACGCATGGA ATTGAACGGG GTGTATGTGG ACACAGAATT CCTGAAAAAG	1560
5	CTCTCGGAGG AGTACGGCAA AAAGCTCGAG GAACTGGCCG AAAAAATCTA CCAGATAGCA	1620
	GGTGAGCCCT TCAACATCAA TTCTCCAAAA CAGGTTTCAA AGATCCTTTT TGAGAAGCTG	1680
	GGAATAAAAC CCCGTGGAAA AACGACAAAA ACAGGAGAGT ACTCTACCAG GATAGAGGTG	1740
	TTGGAAGAGA TAGCGAATGA GCACGAGATA GTACCCCTCA TTCTCGAGTA CAGAAAGATC	1800
	CAGAAACTGA AATCGACCTA CATAGACACC CTTCCGAAAC TTGTGAACCC GAAAACCGGA	1860
10	AGAATTCATG CATCTTTCCA CCAGACGGGT ACCGCCACTG GCAGGTTGAG TAGCAGTGAT	1920
	CCAAATCTTC AGAATCTTCC GACAAAGAGC GAAGAGGGAA AAGAAATTAG AAAAGCGATT	1980
	GTGCCCCAGG ATCCAGACTG GTGGATCGTC AGTGCGGATT ATTCCCAAAT AGAACTCAGA	2040
	ATCCTCGCTC ATCTCAGTGG TGATGAGAAC CTTGTGAAGG CCTTCGAGGA GGGCATCGAT	2100
	GTGCACACCT TGA CTGCCTC CAGGATCTAC AACGTAAAGC CAGAAGAAGT GAACGAAGAA	2160
15	ATGCGACGGG TTGGAAAGAT GGTGAACTTC TCTATAATAT ACGGTGTCAC ACCGTACGGT	2220
	CTTTCTGTGA GACTTGGAAT ACCGGTTAAA GAAGCAGAAA AGATGATTAT CAGCTATTTT	2280
	ACACTGTATC CAAAGGTGCG AAGCTACATC CAGCAGGTTG TTGCAGAGGC AAAAGAGAAG	2340
	GGCTACGTCA GGA CTCTCTT TGGAAGAAAA AGAGATATTC CCCAGCTCAT GGCAAGGGAC	2400
	AAGAACACCC AGTCCGAAGG CGAAAGAATC GCAATAAACA CCCCCATTCA GGAACGGCG	2460
20	GCAGATATAA TAAAATTGGC TATGATAGAT ATAGACGAGG AGCTGAGAAA AAGAAACATG	2520
	AAATCCAGAA TGATCATTCA GGTTCATGAC GAACTGGTCT TCGAGGTTCC CGATGAGGAA	2580
	AAAGAAGAAC TAGTTGATCT GGTGAAGAAC AAAATGACAA ATGTGGTGAA ACTCTCTGTG	2640
	CCTCTTGAGG TTGACATAAG CATCGGAAAA AGCTGGTCTT GA	2682

(2) INFORMATION FOR SEQ ID NO:2:

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 893 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Arg Leu Phe Leu Phe Asp Gly Thr Ala Leu Ala Tyr Arg Ala  
 1 5 10 15  
 5 Tyr Tyr Ala Leu Asp Arg Ser Leu Ser Thr Ser Thr Gly Ile Pro Thr  
 20 25 30  
 Asn Ala Val Tyr Gly Val Ala Arg Met Leu Val Lys Phe Ile Lys Glu  
 35 40 45  
 10 His Ile Ile Pro Glu Lys Asp Tyr Ala Ala Val Ala Phe Asp Lys Lys  
 50 55 60  
 Ala Ala Thr Phe Arg His Lys Leu Leu Val Ser Asp Lys Ala Gln Arg  
 65 70 75 80  
 Pro Lys Thr Pro Ala Leu Leu Val Gln Gln Leu Pro Tyr Ile Lys Arg  
 85 90 95  
 15 Leu Ile Glu Ala Leu Gly Phe Lys Val Leu Glu Leu Glu Gly Tyr Glu  
 100 105 110  
 Ala Asp Asp Ile Ile Ala Thr Leu Ala Val Arg Ala Ala Arg Phe Leu  
 115 120 125  
 20 Met Arg Phe Ser Leu Ile Thr Gly Asp Lys Asp Met Leu Gln Leu Val  
 130 135 140  
 Asn Glu Lys Ile Lys Val Trp Arg Ile Val Lys Gly Ile Ser Asp Leu  
 145 150 155 160  
 Glu Leu Tyr Asp Ser Lys Lys Val Lys Glu Arg Tyr Gly Val Glu Pro  
 165 170 175  
 25 His Gln Ile Pro Asp Leu Leu Ala Leu Thr Gly Asp Asp Ile Asp Asn  
 180 185 190  
 Ile Pro Gly Val Thr Gly Ile Gly Glu Lys Thr Ala Val Gln Leu Leu  
 195 200 205  
 30 Gly Lys Tyr Arg Asn Leu Glu Tyr Ile Leu Glu His Ala Arg Glu Leu  
 210 215 220  
 Pro Gln Arg Val Arg Lys Ala Leu Leu Arg Asp Arg Glu Val Ala Ile  
 225 230 235 240  
 Leu Ser Lys Lys Leu Ala Thr Leu Val Thr Asn Ala Pro Val Glu Val  
 245 250 255

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Asp Trp Glu Glu Met Lys Tyr Arg Gly Tyr Asp Lys Arg Lys Leu Leu  
 260 265 270  
 Pro Ile Leu Lys Glu Leu Glu Phe Ala Ser Ile Met Lys Glu Leu Gln  
 275 280 285  
 5 Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu Ile Val Lys Asp His  
 290 295 300  
 Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys Glu Val Pro Ser Phe  
 305 310 315 320  
 10 Ala Leu Asp Leu Glu Thr Ser Ser Leu Asp Pro Phe Asn Cys Glu Ile  
 325 330 335  
 Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr Ala Tyr Tyr Ile Pro  
 340 345 350  
 Leu His His Arg Asn Ala Gln Asn Leu Asp Glu Thr Leu Val Leu Ser  
 355 360 365  
 15 Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser Lys Ile Val Gly Gln  
 370 375 380  
 Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val Lys Gly Ile Ser Pro  
 385 390 395 400  
 20 Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala Tyr Leu Leu Glu Pro  
 405 410 415  
 Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser Leu Lys Phe Leu Gly  
 420 425 430  
 Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser Phe Ser Ser Pro Leu  
 435 440 445  
 25 Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp Lys Ala Ala Asn Tyr  
 450 455 460  
 Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu Tyr Lys Ile Leu Ser  
 465 470 475 480  
 30 Met Lys Leu His Glu Ala Glu Leu Glu Asn Val Phe Tyr Arg Ile Glu  
 485 490 495  
 Met Pro Leu Val Asn Val Leu Ala Arg Met Glu Leu Asn Gly Val Tyr  
 500 505 510  
 Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu Glu Tyr Gly Lys Lys  
 515 520 525  
 35 Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile Ala Gly Glu Pro Phe  
 530 535 540  
 Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile Leu Phe Glu Lys Leu

000013330 062701  
 000013330 062701

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His Asp Glu Leu Val Phe Glu Val Pro Asp Glu Glu Lys Glu Glu Leu  
850 855 860

Val Asp Leu Val Lys Asn Lys Met Thr Asn Val Val Lys Leu Ser Val  
865 870 875 880

5 Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser Trp Ser  
885 890

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 677 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Ser Leu His Ala Arg Glu Leu Pro Gln Arg Val Arg Lys Ala Leu  
1 5 10 15

Leu Arg Asp Arg Glu Val Ala Ile Leu Ser Lys Lys Leu Ala Thr Leu  
20 25 30

Val Thr Asn Ala Pro Val Glu Val Asp Trp Glu Glu Met Lys Tyr Arg  
35 40 45

Gly Tyr Asp Lys Arg Lys Leu Leu Pro Ile Leu Lys Glu Leu Glu Phe  
50 55 60

Ala Ser Ile Met Lys Glu Leu Gln Leu Tyr Glu Glu Ala Glu Pro Thr  
65 70 75 80

Gly Tyr Glu Ile Val Lys Asp His Lys Thr Phe Glu Asp Leu Ile Glu  
85 90 95

Lys Leu Lys Glu Val Pro Ser Phe Ala Leu Ala Leu Glu Thr Ser Ser  
100 105 110

Leu Asp Pro Phe Asn Cys Glu Ile Val Gly Ile Ser Val Ser Phe Lys  
115 120 125

Pro Lys Thr Ala Tyr Tyr Ile Pro Leu His His Arg Asn Ala Gln Asn  
130 135 140

Leu Asp Glu Thr Leu Val Leu Ser Lys Leu Lys Glu Ile Leu Glu Asp  
145 150 155 160

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Pro	Ser	Ser	Lys	Ile	Val	Gly	Gln	Asn	Leu	Lys	Tyr	Asp	Tyr	Lys	Val	165	170	175
Leu	Met	Val	Lys	Gly	Ile	Ser	Pro	Val	Tyr	Pro	His	Phe	Asp	Thr	Met	180	185	190
Ile	Ala	Ala	Tyr	Leu	Leu	Glu	Pro	Asn	Glu	Lys	Lys	Phe	Asn	Leu	Glu	195	200	205
Asp	Leu	Ser	Leu	Lys	Phe	Leu	Gly	Tyr	Lys	Met	Thr	Ser	Tyr	Gln	Glu	210	215	220
Leu	Met	Ser	Phe	Ser	Ser	Pro	Leu	Phe	Gly	Phe	Ser	Phe	Ala	Asp	Val	225	230	235
Pro	Val	Asp	Lys	Ala	Ala	Asn	Tyr	Ser	Cys	Glu	Asp	Ala	Asp	Ile	Thr	245	250	255
Tyr	Arg	Leu	Tyr	Lys	Ile	Leu	Ser	Met	Lys	Leu	His	Glu	Ala	Glu	Leu	260	265	270
Glu	Asn	Val	Phe	Tyr	Arg	Ile	Glu	Met	Pro	Leu	Val	Asn	Val	Leu	Ala	275	280	285
Arg	Met	Glu	Leu	Asn	Gly	Val	Tyr	Val	Asp	Thr	Glu	Phe	Leu	Lys	Lys	290	295	300
Leu	Ser	Glu	Glu	Tyr	Gly	Lys	Lys	Leu	Glu	Glu	Leu	Ala	Glu	Lys	Ile	305	310	315
Tyr	Gln	Ile	Ala	Gly	Glu	Pro	Phe	Asn	Ile	Asn	Ser	Pro	Lys	Gln	Val	325	330	335
Ser	Lys	Ile	Leu	Phe	Glu	Lys	Leu	Gly	Ile	Lys	Pro	Arg	Gly	Lys	Thr	340	345	350
Thr	Lys	Thr	Gly	Glu	Tyr	Ser	Thr	Arg	Ile	Glu	Val	Leu	Glu	Glu	Ile	355	360	365
Ala	Asn	Glu	His	Glu	Ile	Val	Pro	Leu	Ile	Leu	Glu	Tyr	Arg	Lys	Ile	370	375	380
Gln	Lys	Leu	Lys	Ser	Thr	Tyr	Ile	Asp	Thr	Leu	Pro	Lys	Leu	Val	Asn	385	390	395
Pro	Lys	Thr	Gly	Arg	Ile	His	Ala	Ser	Phe	His	Gln	Thr	Gly	Thr	Ala	405	410	415
Thr	Gly	Arg	Leu	Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Leu	Pro	Thr	420	425	430
Lys	Ser	Glu	Glu	Gly	Lys	Glu	Ile	Arg	Lys	Ala	Ile	Val	Pro	Gln	Asp	435	440	445
Pro	Asp	Trp	Trp	Ile	Val	Ser	Ala	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg			

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450                      455                      460  
 Ile Leu Ala His Leu Ser Gly Asp Glu Asn Leu Val Lys Ala Phe Glu  
 465                      470                      475                      480  
 5    Glu Gly Ile Asp Val His Thr Leu Thr Ala Ser Arg Ile Tyr Asn Val  
                                  485                      490                      495  
 Lys Pro Glu Glu Val Asn Glu Glu Met Arg Arg Val Gly Lys Met Val  
                                  500                      505                      510  
 Asn Phe Ser Ile Ile Tyr Gly Val Thr Pro Tyr Gly Leu Ser Val Arg  
                                  515                      520                      525  
 10    Leu Gly Ile Pro Val Lys Glu Ala Glu Lys Met Ile Ile Ser Tyr Phe  
                                  530                      535                      540  
 Thr Leu Tyr Pro Lys Val Arg Ser Tyr Ile Gln Gln Val Val Ala Glu  
 545                      550                      555                      560  
 15    Ala Lys Glu Lys Gly Tyr Val Arg Thr Leu Phe Gly Arg Lys Arg Asp  
                                  565                      570                      575  
 Ile Pro Gln Leu Met Ala Arg Asp Lys Asn Thr Gln Ser Glu Gly Glu  
                                  580                      585                      590  
 Arg Ile Ala Ile Asn Thr Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile  
                                  595                      600                      605  
 20    Lys Leu Ala Met Ile Asp Ile Asp Glu Glu Leu Arg Lys Arg Asn Met  
                                  610                      615                      620  
 Lys Ser Arg Met Ile Ile Gln Val His Asp Glu Leu Val Phe Glu Val  
 625                      630                      635                      640  
 25    Pro Asp Glu Glu Lys Glu Glu Leu Val Asp Leu Val Lys Asn Lys Met  
                                  645                      650                      655  
 Thr Asn Val Val Lys Leu Ser Val Pro Leu Glu Val Asp Ile Ser Ile  
                                  660                      665                      670  
 Gly Lys Ser Trp Ser  
                                  675

30    (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- 35    (A) LENGTH: 610 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

	Met	Lys	Glu	Leu	Gln	Leu	Tyr	Glu	Glu	Ala	Glu	Pro	Thr	Gly	Tyr	Glu	
	1				5					10					15		
5	Ile	Val	Lys	Asp	His	Lys	Thr	Phe	Glu	Asp	Leu	Ile	Glu	Lys	Leu	Lys	
				20					25					30			
	Glu	Val	Pro	Ser	Phe	Ala	Leu	Ala	Leu	Glu	Thr	Ser	Ser	Leu	Asp	Pro	
			35					40					45				
	Phe	Asn	Cys	Glu	Ile	Val	Gly	Ile	Ser	Val	Ser	Phe	Lys	Pro	Lys	Thr	
		50					55					60					
10	Ala	Tyr	Tyr	Ile	Pro	Leu	His	His	Arg	Asn	Ala	Gln	Asn	Leu	Asp	Glu	
	65					70				75					80		
	Thr	Leu	Val	Leu	Ser	Lys	Leu	Lys	Glu	Ile	Leu	Glu	Asp	Pro	Ser	Ser	
					85					90					95		
15	Lys	Ile	Val	Gly	Gln	Asn	Leu	Lys	Tyr	Asp	Tyr	Lys	Val	Leu	Met	Val	
				100					105					110			
	Lys	Gly	Ile	Ser	Pro	Val	Tyr	Pro	His	Phe	Asp	Thr	Met	Ile	Ala	Ala	
			115					120					125				
	Tyr	Leu	Leu	Glu	Pro	Asn	Glu	Lys	Lys	Phe	Asn	Leu	Glu	Asp	Leu	Ser	
		130					135					140					
20	Leu	Lys	Phe	Leu	Gly	Tyr	Lys	Met	Thr	Ser	Tyr	Gln	Glu	Leu	Met	Ser	
	145					150					155				160		
	Phe	Ser	Ser	Pro	Leu	Phe	Gly	Phe	Ser	Phe	Ala	Asp	Val	Pro	Val	Asp	
					165					170					175		
25	Lys	Ala	Ala	Asn	Tyr	Ser	Cys	Glu	Asp	Ala	Asp	Ile	Thr	Tyr	Arg	Leu	
				180					185					190			
	Tyr	Lys	Ile	Leu	Ser	Met	Lys	Leu	His	Glu	Ala	Glu	Leu	Glu	Asn	Val	
			195				200						205				
	Phe	Tyr	Arg	Ile	Glu	Met	Pro	Leu	Val	Asn	Val	Leu	Ala	Arg	Met	Glu	
		210				215						220					
30	Leu	Asn	Gly	Val	Tyr	Val	Asp	Thr	Glu	Phe	Leu	Lys	Lys	Leu	Ser	Glu	
	225					230					235				240		
	Glu	Tyr	Gly	Lys	Lys	Leu	Glu	Glu	Leu	Ala	Glu	Lys	Ile	Tyr	Gln	Ile	
					245					250				255			
35	Ala	Gly	Glu	Pro	Phe	Asn	Ile	Asn	Ser	Pro	Lys	Gln	Val	Ser	Lys	Ile	
				260				265						270			
	Leu	Phe	Glu	Lys	Leu	Gly	Ile	Lys	Pro	Arg	Gly	Lys	Thr	Thr	Lys	Thr	

285

Met Ile Ile Gln Val His Asp Glu Leu Val Phe Glu Val Pro Asp Glu

565 570 575

Glu Lys Glu Glu Leu Val Asp Leu Val Lys Asn Lys Met Thr Asn Val  
580 585 590

Val Lys Leu Ser Val Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser  
595 600 605

Trp Ser  
610

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 708 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Asn Ser Ser Ser Val Pro Ile Pro Gly Val Thr Gly Ile Gly Glu  
1 5 10 15

Lys Thr Ala Val Gln Leu Leu Gly Lys Tyr Arg Asn Leu Glu Tyr Ile  
20 25 30

Leu Glu His Ala Arg Glu Leu Pro Gln Arg Val Arg Lys Ala Leu Leu  
35 40 45

Arg Asp Arg Glu Val Ala Ile Leu Ser Lys Lys Leu Ala Thr Leu Val  
50 55 60

Thr Asn Ala Pro Val Glu Val Asp Trp Glu Glu Met Lys Tyr Arg Gly  
65 70 75 80

Tyr Asp Lys Arg Lys Leu Leu Pro Ile Leu Lys Glu Leu Glu Phe Ala  
85 90 95

Ser Ile Met Lys Glu Leu Gln Leu Tyr Glu Glu Ala Glu Pro Thr Gly  
100 105 110

Tyr Glu Ile Val Lys Asp His Lys Thr Phe Glu Asp Leu Ile Glu Lys  
115 120 125

Leu Lys Glu Val Pro Ser Phe Ala Leu Ala Leu Glu Thr Ser Ser Leu  
130 135 140

Asp Pro Phe Asn Cys Glu Ile Val Gly Ile Ser Val Ser Phe Lys Pro

145                      150                      155                      160  
 Lys Thr Ala Tyr Tyr Ile Pro Leu His His Arg Asn Ala Gln Asn Leu  
                                  165                      170                      175  
 5 Asp Glu Thr Leu Val Leu Ser Lys Leu Lys Glu Ile Leu Glu Asp Pro  
                                  180                      185                      190  
 Ser Ser Lys Ile Val Gly Gln Asn Leu Lys Tyr Asp Tyr Lys Val Leu  
                                  195                      200                      205  
 Met Val Lys Gly Ile Ser Pro Val Tyr Pro His Phe Asp Thr Met Ile  
                                  210                      215                      220  
 10 Ala Ala Tyr Leu Leu Glu Pro Asn Glu Lys Lys Phe Asn Leu Glu Asp  
                                  225                      230                      235                      240  
 Leu Ser Leu Lys Phe Leu Gly Tyr Lys Met Thr Ser Tyr Gln Glu Leu  
                                  245                      250                      255  
 15 Met Ser Phe Ser Ser Pro Leu Phe Gly Phe Ser Phe Ala Asp Val Pro  
                                  260                      265                      270  
 Val Asp Lys Ala Ala Asn Tyr Ser Cys Glu Asp Ala Asp Ile Thr Tyr  
                                  275                      280                      285  
 Arg Leu Tyr Lys Ile Leu Ser Met Lys Leu His Glu Ala Glu Leu Glu  
                                  290                      295                      300  
 20 Asn Val Phe Tyr Arg Ile Glu Met Pro Leu Val Asn Val Leu Ala Arg  
                                  305                      310                      315                      320  
 Met Glu Leu Asn Gly Val Tyr Val Asp Thr Glu Phe Leu Lys Lys Leu  
                                  325                      330                      335  
 25 Ser Glu Glu Tyr Gly Lys Lys Leu Glu Glu Leu Ala Glu Lys Ile Tyr  
                                  340                      345                      350  
 Gln Ile Ala Gly Glu Pro Phe Asn Ile Asn Ser Pro Lys Gln Val Ser  
                                  355                      360                      365  
 Lys Ile Leu Phe Glu Lys Leu Gly Ile Lys Pro Arg Gly Lys Thr Thr  
                                  370                      375                      380  
 30 Lys Thr Gly Glu Tyr Ser Thr Arg Ile Glu Val Leu Glu Glu Ile Ala  
                                  385                      390                      395                      400  
 Asn Glu His Glu Ile Val Pro Leu Ile Leu Glu Tyr Arg Lys Ile Gln  
                                  405                      410                      415  
 35 Lys Leu Lys Ser Thr Tyr Ile Asp Thr Leu Pro Lys Leu Val Asn Pro  
                                  420                      425                      430  
 Lys Thr Gly Arg Ile His Ala Ser Phe His Gln Thr Gly Thr Ala Thr

		435							440							445						
	Gly	Arg	Leu	Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Leu	Pro	Thr	Lys						
	450						455					460										
5	Ser	Glu	Glu	Gly	Lys	Glu	Ile	Arg	Lys	Ala	Ile	Val	Pro	Gln	Asp	Pro						
	465					470					475					480						
	Asp	Trp	Trp	Ile	Val	Ser	Ala	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Ile						
					485					490					495							
	Leu	Ala	His	Leu	Ser	Gly	Asp	Glu	Asn	Leu	Val	Lys	Ala	Phe	Glu	Glu						
				500					505					510								
10	Gly	Ile	Asp	Val	His	Thr	Leu	Thr	Ala	Ser	Arg	Ile	Tyr	Asn	Val	Lys						
			515					520					525									
	Pro	Glu	Glu	Val	Asn	Glu	Glu	Met	Arg	Arg	Val	Gly	Lys	Met	Val	Asn						
		530					535					540										
15	Phe	Ser	Ile	Ile	Tyr	Gly	Val	Thr	Pro	Tyr	Gly	Leu	Ser	Val	Arg	Leu						
	545					550					555					560						
	Gly	Ile	Pro	Val	Lys	Glu	Ala	Glu	Lys	Met	Ile	Ile	Ser	Tyr	Phe	Thr						
					565					570					575							
	Leu	Tyr	Pro	Lys	Val	Arg	Ser	Tyr	Ile	Gln	Gln	Val	Val	Ala	Glu	Ala						
				580					585					590								
20	Lys	Glu	Lys	Gly	Tyr	Val	Arg	Thr	Leu	Phe	Gly	Arg	Lys	Arg	Asp	Ile						
		595						600					605									
	Pro	Gln	Leu	Met	Ala	Arg	Asp	Lys	Asn	Thr	Gln	Ser	Glu	Gly	Glu	Arg						
		610					615					620										
25	Ile	Ala	Ile	Asn	Thr	Pro	Ile	Gln	Gly	Thr	Ala	Ala	Asp	Ile	Ile	Lys						
	625					630					635					640						
	Leu	Ala	Met	Ile	Asp	Ile	Asp	Glu	Glu	Leu	Arg	Lys	Arg	Asn	Met	Lys						
					645					650					655							
	Ser	Arg	Met	Ile	Ile	Gln	Val	His	Asp	Glu	Leu	Val	Phe	Glu	Val	Pro						
				660					665					670								
30	Asp	Glu	Glu	Lys	Glu	Glu	Leu	Val	Asp	Leu	Val	Lys	Asn	Lys	Met	Thr						
		675						680					685									
	Asn	Val	Val	Lys	Leu	Ser	Val	Pro	Leu	Glu	Val	Asp	Ile	Ser	Ile	Gly						
		690					695					700										
35	Lys	Ser	Trp	Ser																		
	705																					

(2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 893 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: not relevant

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## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ala Arg Leu Phe Leu Phe Asp Gly Thr Ala Leu Ala Tyr Arg Ala  
 1 5 10 15

10 Tyr Tyr Ala Leu Asp Arg Ser Leu Ser Thr Ser Thr Gly Ile Pro Thr  
 20 25 30

Asn Ala Val Tyr Gly Val Ala Arg Met Leu Val Lys Phe Ile Lys Glu  
 35 40 45

15 His Ile Ile Pro Glu Lys Asp Tyr Ala Ala Val Ala Phe Asp Lys Lys  
 50 55 60

Ala Ala Thr Phe Arg His Lys Leu Leu Val Ser Asp Lys Ala Gln Arg  
 65 70 75 80

Pro Lys Thr Pro Ala Leu Leu Val Gln Gln Leu Pro Tyr Ile Lys Arg  
 85 90 95

20 Leu Ile Glu Ala Leu Gly Phe Lys Val Leu Glu Leu Glu Gly Tyr Glu  
 100 105 110

Ala Asp Asp Ile Ile Ala Thr Leu Ala Val Arg Ala Ala Arg Phe Leu  
 115 120 125

25 Met Arg Phe Ser Leu Ile Thr Gly Ala Lys Asp Met Leu Gln Leu Val  
 130 135 140

Asn Glu Lys Ile Lys Val Trp Arg Ile Val Lys Gly Ile Ser Asp Leu  
 145 150 155 160

Glu Leu Tyr Asp Ser Lys Lys Val Lys Glu Arg Tyr Gly Val Glu Pro  
 165 170 175

30 His Gln Ile Pro Asp Leu Leu Ala Leu Thr Gly Asp Asp Ile Asp Asn  
 180 185 190

Ile Pro Gly Val Thr Gly Ile Gly Glu Lys Thr Ala Val Gln Leu Leu  
 195 200 205

35 Gly Lys Tyr Arg Asn Leu Glu Tyr Ile Leu Glu His Ala Arg Glu Leu  
 210 215 220

Pro Gln Arg Val Arg Lys Ala Leu Leu Arg Asp Arg Glu Val Ala Ile  
 225 230 235 240  
 Leu Ser Lys Lys Leu Ala Thr Leu Val Thr Asn Ala Pro Val Glu Val  
 245 250 255  
 5 Asp Trp Glu Glu Met Lys Tyr Arg Gly Tyr Asp Lys Arg Lys Leu Leu  
 260 265 270  
 Pro Ile Leu Lys Glu Leu Glu Phe Ala Ser Ile Met Lys Glu Leu Gln  
 275 280 285  
 10 Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu Ile Val Lys Asp His  
 290 295 300  
 Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys Glu Val Pro Ser Phe  
 305 310 315 320  
 Ala Leu Ala Leu Glu Thr Ser Ser Leu Asp Pro Phe Asn Cys Glu Ile  
 325 330 335  
 15 Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr Ala Tyr Tyr Ile Pro  
 340 345 350  
 Leu His His Arg Asn Ala Gln Asn Leu Asp Glu Thr Leu Val Leu Ser  
 355 360 365  
 20 Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser Lys Ile Val Gly Gln  
 370 375 380  
 Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val Lys Gly Ile Ser Pro  
 385 390 395 400  
 Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala Tyr Leu Leu Glu Pro  
 405 410 415  
 25 Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser Leu Lys Phe Leu Gly  
 420 425 430  
 Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser Phe Ser Ser Pro Leu  
 435 440 445  
 30 Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp Lys Ala Ala Asn Tyr  
 450 455 460  
 Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu Tyr Lys Ile Leu Ser  
 465 470 475 480  
 Met Lys Leu His Glu Ala Glu Leu Glu Asn Val Phe Tyr Arg Ile Glu  
 485 490 495  
 35 Met Pro Leu Val Asn Val Leu Ala Arg Met Glu Leu Asn Gly Val Tyr  
 500 505 510



	Val	Asp	Thr	Glu	Phe	Leu	Lys	Lys	Leu	Ser	Glu	Glu	Tyr	Gly	Lys	Lys	
		515						520						525			
	Leu	Glu	Glu	Leu	Ala	Glu	Lys	Ile	Tyr	Gln	Ile	Ala	Gly	Glu	Pro	Phe	
		530					535					540					
5	Asn	Ile	Asn	Ser	Pro	Lys	Gln	Val	Ser	Lys	Ile	Leu	Phe	Glu	Lys	Leu	
	545					550					555					560	
	Gly	Ile	Lys	Pro	Arg	Gly	Lys	Thr	Thr	Lys	Thr	Gly	Glu	Tyr	Ser	Thr	
					565					570					575		
10	Arg	Ile	Glu	Val	Leu	Glu	Glu	Ile	Ala	Asn	Glu	His	Glu	Ile	Val	Pro	
				580					585					590			
	Leu	Ile	Leu	Glu	Tyr	Arg	Lys	Ile	Gln	Lys	Leu	Lys	Ser	Thr	Tyr	Ile	
			595					600					605				
	Asp	Thr	Leu	Pro	Lys	Leu	Val	Asn	Pro	Lys	Thr	Gly	Arg	Ile	His	Ala	
		610					615					620					
15	Ser	Phe	His	Gln	Thr	Gly	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser	Ser	Asp	
	625					630					635					640	
	Pro	Asn	Leu	Gln	Asn	Leu	Pro	Thr	Lys	Ser	Glu	Glu	Gly	Lys	Glu	Ile	
					645					650					655		
20	Arg	Lys	Ala	Ile	Val	Pro	Gln	Asp	Pro	Asp	Trp	Trp	Ile	Val	Ser	Ala	
				660					665					670			
	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Ile	Leu	Ala	His	Leu	Ser	Gly	Asp	
			675					680					685				
	Glu	Asn	Leu	Val	Lys	Ala	Phe	Glu	Glu	Gly	Ile	Asp	Val	His	Thr	Leu	
		690					695					700					
25	Thr	Ala	Ser	Arg	Ile	Tyr	Asn	Val	Lys	Pro	Glu	Glu	Val	Asn	Glu	Glu	
	705					710					715					720	
	Met	Arg	Arg	Val	Gly	Lys	Met	Val	Asn	Phe	Ser	Ile	Ile	Tyr	Gly	Val	
					725					730					735		
30	Thr	Pro	Tyr	Gly	Leu	Ser	Val	Arg	Leu	Gly	Ile	Pro	Val	Lys	Glu	Ala	
				740					745					750			
	Glu	Lys	Met	Ile	Ile	Ser	Tyr	Phe	Thr	Leu	Tyr	Pro	Lys	Val	Arg	Ser	
			755					760					765				
	Tyr	Ile	Gln	Gln	Val	Val	Ala	Glu	Ala	Lys	Glu	Lys	Gly	Tyr	Val	Arg	
		770					775					780					
35	Thr	Leu	Phe	Gly	Arg	Lys	Arg	Asp	Ile	Pro	Gln	Leu	Met	Ala	Arg	Asp	
	785					790					795					800	

Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala Ile Asn Thr Pro Ile  
805 810 815

Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asp Ile Asp  
820 825 830

5 Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg Met Ile Ile Gln Val  
835 840 845

His Asp Glu Leu Val Phe Glu Val Pro Asp Glu Glu Lys Glu Glu Leu  
850 855 860

10 Val Asp Leu Val Lys Asn Lys Met Thr Asn Val Val Lys Leu Ser Val  
865 870 875 880

Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser Trp Ser  
885 890

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 893 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Arg Leu Phe Leu Phe Ala Gly Thr Ala Leu Ala Tyr Arg Ala  
1 5 10 15

Tyr Tyr Ala Leu Asp Arg Ser Leu Ser Thr Ser Thr Gly Ile Pro Thr  
20 25 30

25 Asn Ala Val Tyr Gly Val Ala Arg Met Leu Val Lys Phe Ile Lys Glu  
35 40 45

His Ile Ile Pro Glu Lys Asp Tyr Ala Ala Val Ala Phe Asp Lys Lys  
50 55 60

30 Ala Ala Thr Phe Arg His Lys Leu Leu Val Ser Asp Lys Ala Gln Arg  
65 70 75 80

Pro Lys Thr Pro Ala Leu Leu Val Gln Gln Leu Pro Tyr Ile Lys Arg  
85 90 95

Leu Ile Glu Ala Leu Gly Phe Lys Val Leu Glu Leu Glu Gly Tyr Glu  
100 105 110

35 Ala Asp Asp Ile Ile Ala Thr Leu Ala Val Arg Ala Ala Arg Phe Leu

	115	120	125
	Met Arg Phe Ser Leu Ile Thr Gly Asp Lys Asp Met Leu Gln Leu Val 130 135 140		
5	Asn Glu Lys Ile Lys Val Trp Arg Ile Val Lys Gly Ile Ser Asp Leu 145 150 155 160		
	Glu Leu Tyr Asp Ser Lys Lys Val Lys Glu Arg Tyr Gly Val Glu Pro 165 170 175		
	His Gln Ile Pro Asp Leu Leu Ala Leu Thr Gly Asp Asp Ile Asp Asn 180 185 190		
10	Ile Pro Gly Val Thr Gly Ile Gly Glu Lys Thr Ala Val Gln Leu Leu 195 200 205		
	Gly Lys Tyr Arg Asn Leu Glu Tyr Ile Leu Glu His Ala Arg Glu Leu 210 215 220		
15	Pro Gln Arg Val Arg Lys Ala Leu Leu Arg Asp Arg Glu Val Ala Ile 225 230 235 240		
	Leu Ser Lys Lys Leu Ala Thr Leu Val Thr Asn Ala Pro Val Glu Val 245 250 255		
	Asp Trp Glu Glu Met Lys Tyr Arg Gly Tyr Asp Lys Arg Lys Leu Leu 260 265 270		
20	Pro Ile Leu Lys Glu Leu Glu Phe Ala Ser Ile Met Lys Glu Leu Gln 275 280 285		
	Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu Ile Val Lys Asp His 290 295 300		
25	Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys Glu Val Pro Ser Phe 305 310 315 320		
	Ala Leu Ala Leu Glu Thr Ser Ser Leu Asp Pro Phe Asn Cys Glu Ile 325 330 335		
	Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr Ala Tyr Tyr Ile Pro 340 345 350		
30	Leu His His Arg Asn Ala Gln Asn Leu Asp Glu Thr Leu Val Leu Ser 355 360 365		
	Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser Lys Ile Val Gly Gln 370 375 380		
35	Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val Lys Gly Ile Ser Pro 385 390 395 400		
	Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala Tyr Leu Leu Glu Pro 405 410 415		

Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser Leu Lys Phe Leu Gly  
 420 425 430  
 Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser Phe Ser Ser Pro Leu  
 435 440 445  
 5 Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp Lys Ala Ala Asn Tyr  
 450 455 460  
 Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu Tyr Lys Ile Leu Ser  
 465 470 475 480  
 10 Met Lys Leu His Glu Ala Glu Leu Glu Asn Val Phe Tyr Arg Ile Glu  
 485 490 495  
 Met Pro Leu Val Asn Val Leu Ala Arg Met Glu Leu Asn Gly Val Tyr  
 500 505 510  
 Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu Glu Tyr Gly Lys Lys  
 515 520 525  
 15 Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile Ala Gly Glu Pro Phe  
 530 535 540  
 Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile Leu Phe Glu Lys Leu  
 545 550 555 560  
 20 Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr Gly Glu Tyr Ser Thr  
 565 570 575  
 Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu His Glu Ile Val Pro  
 580 585 590  
 Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu Lys Ser Thr Tyr Ile  
 595 600 605  
 25 Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr Gly Arg Ile His Ala  
 610 615 620  
 Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp  
 625 630 635 640  
 30 Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu Glu Gly Lys Glu Ile  
 645 650 655  
 Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp Trp Ile Val Ser Ala  
 660 665 670  
 Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala His Leu Ser Gly Asp  
 675 680 685  
 35 Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile Asp Val His Thr Leu  
 690 695 700

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 10/29/90 12:16:50

Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu Glu Val Asn Glu Glu  
705 710 715 720

Met Arg Arg Val Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly Val  
725 730 735

5 Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile Pro Val Lys Glu Ala  
740 745 750

Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr Pro Lys Val Arg Ser  
755 760 765

10 Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu Lys Gly Tyr Val Arg  
770 775 780

Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln Leu Met Ala Arg Asp  
785 790 795 800

Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala Ile Asn Thr Pro Ile  
805 810 815

15 Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asp Ile Asp  
820 825 830

Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg Met Ile Ile Gln Val  
835 840 845

20 His Asp Glu Leu Val Phe Glu Val Pro Asp Glu Glu Lys Glu Glu Leu  
850 855 860

Val Asp Leu Val Lys Asn Lys Met Thr Asn Val Val Lys Leu Ser Val  
865 870 875 880

Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser Trp Ser  
885 890

25 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 893 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: not relevant

30

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ala Arg Leu Phe Leu Phe Asp Gly Thr Ala Leu Ala Tyr Arg Ala  
1 5 10 15

000133-0001

Tyr Tyr Ala Leu Asp Arg Ser Leu Ser Thr Ser Thr Gly Ile Pro Thr  
 20 25 30  
 Asn Ala Val Tyr Gly Val Ala Arg Met Leu Val Lys Phe Ile Lys Glu  
 35 40 45  
 5 His Ile Ile Pro Glu Lys Asp Tyr Ala Ala Val Ala Phe Asp Lys Lys  
 50 55 60  
 Ala Ala Thr Phe Arg His Lys Leu Leu Val Ser Asp Lys Ala Gln Arg  
 65 70 75 80  
 10 Pro Lys Thr Pro Ala Leu Leu Val Gln Gln Leu Pro Tyr Ile Lys Arg  
 85 90 95  
 Leu Ile Glu Ala Leu Gly Phe Lys Val Leu Glu Leu Glu Gly Tyr Glu  
 100 105 110  
 Ala Asp Asp Ile Ile Ala Thr Leu Ala Val Arg Ala Ala Arg Phe Leu  
 115 120 125  
 15 Met Arg Phe Ser Leu Ile Thr Gly Asp Lys Asp Met Leu Gln Leu Val  
 130 135 140  
 Asn Glu Lys Ile Lys Val Trp Arg Ile Val Lys Gly Ile Ser Asp Leu  
 145 150 155 160  
 20 Glu Leu Tyr Asp Ser Lys Lys Val Lys Glu Arg Tyr Gly Val Glu Pro  
 165 170 175  
 His Gln Ile Pro Asp Leu Leu Ala Leu Thr Gly Asp Asp Ile Asp Asn  
 180 185 190  
 Ile Pro Asp Val Thr Gly Ile Gly Glu Lys Thr Ala Val Gln Leu Leu  
 195 200 205  
 25 Gly Lys Tyr Arg Asn Leu Glu Tyr Ile Leu Glu His Ala Arg Glu Leu  
 210 215 220  
 Pro Gln Arg Val Arg Lys Ala Leu Leu Arg Asp Arg Glu Val Ala Ile  
 225 230 235 240  
 30 Leu Ser Lys Lys Leu Ala Thr Leu Val Thr Asn Ala Pro Val Glu Val  
 245 250 255  
 Asp Trp Glu Glu Met Lys Tyr Arg Gly Tyr Asp Lys Arg Lys Leu Leu  
 260 265 270  
 Pro Ile Leu Lys Glu Leu Glu Phe Ala Ser Ile Met Lys Glu Leu Gln  
 275 280 285  
 35 Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu Ile Val Lys Asp His  
 290 295 300

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 10/29/90 22:25:26

Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys Glu Val Pro Ser Phe  
 305 310 315 320  
 Ala Leu Ala Leu Glu Thr Ser Ser Leu Asp Pro Phe Asn Cys Glu Ile  
 325 330 335  
 5 Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr Ala Tyr Tyr Ile Pro  
 340 345 350  
 Leu His His Arg Asn Ala Gln Asn Leu Asp Glu Thr Leu Val Leu Ser  
 355 360 365  
 10 Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser Lys Ile Val Gly Gln  
 370 375 380  
 Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val Lys Gly Ile Ser Pro  
 385 390 395 400  
 Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala Tyr Leu Leu Glu Pro  
 405 410 415  
 15 Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser Leu Lys Phe Leu Gly  
 420 425 430  
 Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser Phe Ser Ser Pro Leu  
 435 440 445  
 20 Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp Lys Ala Ala Asn Tyr  
 450 455 460  
 Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu Tyr Lys Ile Leu Ser  
 465 470 475 480  
 Met Lys Leu His Glu Ala Glu Leu Glu Asn Val Phe Tyr Arg Ile Glu  
 485 490 495  
 25 Met Pro Leu Val Asn Val Leu Ala Arg Met Glu Leu Asn Gly Val Tyr  
 500 505 510  
 Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu Glu Tyr Gly Lys Lys  
 515 520 525  
 30 Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile Ala Gly Glu Pro Phe  
 530 535 540  
 Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile Leu Phe Glu Lys Leu  
 545 550 555 560  
 Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr Gly Glu Tyr Ser Thr  
 565 570 575  
 35 Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu His Glu Ile Val Pro  
 580 585 590

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 10/29/00 2:22:16 PM

Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu Lys Ser Thr Tyr Ile  
 595 600 605  
 Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr Gly Arg Ile His Ala  
 610 615 620  
 5 Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp  
 625 630 635 640  
 Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu Glu Gly Lys Glu Ile  
 645 650 655  
 10 Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp Trp Ile Val Ser Ala  
 660 665 670  
 Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala His Leu Ser Gly Asp  
 675 680 685  
 Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile Asp Val His Thr Leu  
 690 695 700  
 15 Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu Glu Val Asn Glu Glu  
 705 710 715 720  
 Met Arg Arg Val Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly Val  
 725 730 735  
 20 Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile Pro Val Lys Glu Ala  
 740 745 750  
 Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr Pro Lys Val Arg Ser  
 755 760 765  
 Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu Lys Gly Tyr Val Arg  
 770 775 780  
 25 Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln Leu Met Ala Arg Asp  
 785 790 795 800  
 Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala Ile Asn Thr Pro Ile  
 805 810 815  
 30 Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asp Ile Asp  
 820 825 830  
 Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg Met Ile Ile Gln Val  
 835 840 845  
 His Asp Glu Leu Val Phe Glu Val Pro Asp Glu Glu Lys Glu Glu Leu  
 850 855 860  
 35 Val Asp Leu Val Lys Asn Lys Met Thr Asn Val Val Lys Leu Ser Val  
 865 870 875 880

05891332.062701



Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser Trp Ser  
885 890

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 893 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

## 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ala Arg Leu Phe Leu Phe Asp Gly Thr Ala Leu Ala Tyr Arg Ala  
1 5 10 15  
Tyr Tyr Ala Leu Asp Arg Ser Leu Ser Thr Ser Thr Gly Ile Pro Thr  
20 25 30  
Asn Ala Val Tyr Asp Val Ala Arg Met Leu Val Lys Phe Ile Lys Glu  
35 40 45  
His Ile Ile Pro Glu Lys Asp Tyr Ala Ala Val Ala Phe Asp Lys Lys  
50 55 60  
Ala Ala Thr Phe Arg His Lys Leu Leu Val Ser Asp Lys Ala Gln Arg  
65 70 75 80  
Pro Lys Thr Pro Ala Leu Leu Val Gln Gln Leu Pro Tyr Ile Lys Arg  
85 90 95  
Leu Ile Glu Ala Leu Gly Phe Lys Val Leu Glu Leu Glu Gly Tyr Glu  
100 105 110  
Ala Asp Asp Ile Ile Ala Thr Leu Ala Val Arg Ala Ala Arg Phe Leu  
115 120 125  
Met Arg Phe Ser Leu Ile Thr Gly Asp Lys Asp Met Leu Gln Leu Val  
130 135 140  
Asn Glu Lys Ile Lys Val Trp Arg Ile Val Lys Gly Ile Ser Asp Leu  
145 150 155 160  
Glu Leu Tyr Asp Ser Lys Lys Val Lys Glu Arg Tyr Gly Val Glu Pro  
165 170 175  
His Gln Ile Pro Asp Leu Leu Ala Leu Thr Gly Asp Asp Ile Asp Asn  
180 185 190  
Ile Pro Gly Val Thr Gly Ile Gly Glu Lys Thr Ala Val Gln Leu Leu  
195 200 205

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T02290-2EET666

Gly Lys Tyr Arg Asn Leu Glu Tyr Ile Leu Glu His Ala Arg Glu Leu  
 210 215 220  
 Pro Gln Arg Val Arg Lys Ala Leu Leu Arg Asp Arg Glu Val Ala Ile  
 225 230 235 240  
 5 Leu Ser Lys Lys Leu Ala Thr Leu Val Thr Asn Ala Pro Val Glu Val  
 245 250 255  
 Asp Trp Glu Glu Met Lys Tyr Arg Gly Tyr Asp Lys Arg Lys Leu Leu  
 260 265 270  
 10 Pro Ile Leu Lys Glu Leu Glu Phe Ala Ser Ile Met Lys Glu Leu Gln  
 275 280 285  
 Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu Ile Val Lys Asp His  
 290 295 300  
 Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys Glu Val Pro Ser Phe  
 305 310 315 320  
 15 Ala Leu Ala Leu Glu Thr Ser Ser Leu Asp Pro Phe Asn Cys Glu Ile  
 325 330 335  
 Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr Ala Tyr Tyr Ile Pro  
 340 345 350  
 20 Leu His His Arg Asn Ala Gln Asn Leu Asp Glu Thr Leu Val Leu Ser  
 355 360 365  
 Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser Lys Ile Val Gly Gln  
 370 375 380  
 Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val Lys Gly Ile Ser Pro  
 385 390 395 400  
 25 Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala Tyr Leu Leu Glu Pro  
 405 410 415  
 Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser Leu Lys Phe Leu Gly  
 420 425 430  
 30 Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser Phe Ser Ser Pro Leu  
 435 440 445  
 Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp Lys Ala Ala Asn Tyr  
 450 455 460  
 Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu Tyr Lys Ile Leu Ser  
 465 470 475 480  
 35 Met Lys Leu His Glu Ala Glu Leu Glu Asn Val Phe Tyr Arg Ile Glu  
 485 490 495

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 10/22/90 22:26:00

Met Pro Leu Val Asn Val Leu Ala Arg Met Glu Leu Asn Gly Val Tyr  
 500 505 510  
 Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu Glu Tyr Gly Lys Lys  
 515 520 525  
 5 Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile Ala Gly Glu Pro Phe  
 530 535 540  
 Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile Leu Phe Glu Lys Leu  
 545 550 555 560  
 10 Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr Gly Glu Tyr Ser Thr  
 565 570 575  
 Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu His Glu Ile Val Pro  
 580 585 590  
 Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu Lys Ser Thr Tyr Ile  
 595 600 605  
 15 Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr Gly Arg Ile His Ala  
 610 615 620  
 Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp  
 625 630 635 640  
 20 Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu Glu Gly Lys Glu Ile  
 645 650 655  
 Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp Trp Ile Val Ser Ala  
 660 665 670  
 Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala His Leu Ser Gly Asp  
 675 680 685  
 25 Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile Asp Val His Thr Leu  
 690 695 700  
 Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu Glu Val Asn Glu Glu  
 705 710 715 720  
 30 Met Arg Arg Val Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly Val  
 725 730 735  
 Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile Pro Val Lys Glu Ala  
 740 745 750  
 Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr Pro Lys Val Arg Ser  
 755 760 765  
 35 Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu Lys Gly Tyr Val Arg  
 770 775 780

00001330 062701

Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln Leu Met Ala Arg Asp  
785 790 795 800

Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala Ile Asn Thr Pro Ile  
805 810 815

5 Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asp Ile Asp  
820 825 830

Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg Met Ile Ile Gln Val  
835 840 845

10 His Asp Glu Leu Val Phe Glu Val Pro Asp Glu Glu Lys Glu Glu Leu  
850 855 860

Val Asp Leu Val Lys Asn Lys Met Thr Asn Val Val Lys Leu Ser Val  
865 870 875 880

Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser Trp Ser  
885 890

15 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 610 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: not relevant

20 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Lys Glu Leu Gln Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu  
1 5 10 15

25 Ile Val Lys Asp His Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys  
20 25 30

Glu Val Pro Ser Phe Ala Leu Asp Leu Glu Thr Ser Ser Leu Asp Pro  
35 40 45

30 Phe Asn Cys Glu Ile Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr  
50 55 60

Ala Tyr Tyr Ile Pro Leu His His Arg Asn Ala Gln Asn Leu Asp Glu  
65 70 75 80

Thr Leu Val Leu Ser Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser  
85 90 95

35 Lys Ile Val Gly Gln Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val

0089133E 062704

	100	105	110
	Lys Gly Ile Ser Pro Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala 115 120 125		
5	Tyr Leu Leu Glu Pro Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser 130 135 140		
	Leu Lys Phe Leu Gly Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser 145 150 155 160		
	Phe Ser Ser Pro Leu Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp 165 170 175		
10	Lys Ala Ala Asn Tyr Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu 180 185 190		
	Tyr Lys Ile Leu Ser Met Lys Leu His Glu Ala Glu Leu Glu Asn Val 195 200 205		
15	Phe Tyr Arg Ile Glu Met Pro Leu Val Asn Val Leu Ala Arg Met Glu 210 215 220		
	Leu Asn Gly Val Tyr Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu 225 230 235 240		
	Glu Tyr Gly Lys Lys Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile 245 250 255		
20	Ala Gly Glu Pro Phe Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile 260 265 270		
	Leu Phe Glu Lys Leu Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr 275 280 285		
25	Gly Glu Tyr Ser Thr Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu 290 295 300		
	His Glu Ile Val Pro Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu 305 310 315 320		
	Lys Ser Thr Tyr Ile Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr 325 330 335		
30	Gly Arg Ile His Ala Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg 340 345 350		
	Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu 355 360 365		
35	Glu Gly Lys Glu Ile Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp 370 375 380		
	Trp Ile Val Ser Ala Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala 385 390 395 400		

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His Leu Ser Gly Asp Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile  
 405 410 415  
 Asp Val His Thr Leu Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu  
 420 425 430  
 5 Glu Val Asn Glu Glu Met Arg Arg Val Gly Lys Met Val Asn Phe Ser  
 435 440 445  
 Ile Ile Tyr Gly Val Thr Pro Tyr Gly Leu Ser Val Arg Leu Asn Ile  
 450 455 460  
 10 Pro Val Lys Glu Ala Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr  
 465 470 475 480  
 Pro Lys Val Arg Ser Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu  
 485 490 495  
 Lys Gly Tyr Val Arg Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln  
 500 505 510  
 15 Leu Met Ala Arg Asp Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala  
 515 520 525  
 Ile Asn Thr Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala  
 530 535 540  
 20 Met Ile Asp Ile Asp Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg  
 545 550 555 560  
 Met Ile Ile Gln Val His Asp Glu Leu Val Phe Glu Val Pro Asp Glu  
 565 570 575  
 Glu Lys Glu Glu Leu Val Asp Leu Val Lys Asn Lys Met Thr Asn Val  
 580 585 590  
 25 Val Lys Leu Ser Val Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser  
 595 600 605  
 Trp Ser  
 610

## (2) INFORMATION FOR SEQ ID NO:11:

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear
- 35 (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..14
- (D) OTHER INFORMATION: /note= "'Xaa' is any amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

5      Arg Xaa Xaa Xaa Lys Xaa Xaa Xaa Phe Xaa Xaa Xaa Tyr Xaa  
       1                                5                                10

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

15      Arg Arg Ser Ala Lys Ala Ile Asn Phe Gly Leu Ile Tyr Gly  
       1                                5                                10

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

25      Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly  
       1                                5                                10

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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Arg Asp Asn Ala Lys Thr Phe Ile Tyr Gly Phe Leu Tyr Gly  
1 5 10

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Arg Arg Val Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly  
1 5 10

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 14 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Arg Gln Ala Ala Lys Ala Ile Thr Phe Gly Ile Leu Tyr Gly  
1 5 10

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: peptide



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Arg Arg Ala Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly  
 1 5 10

## (2) INFORMATION FOR SEQ ID NO:18:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 11 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: linear

- 10 (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Pro Ser Phe Ala Leu Asp Leu Glu Thr Ser Ser  
 1 5 10

## (2) INFORMATION FOR SEQ ID NO:19:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 11 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: linear

- 20 (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Pro Val Phe Ala Phe Asp Thr Glu Thr Asp Ser  
 1 5 10

## (2) INFORMATION FOR SEQ ID NO:20:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 11 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: linear

- 30 (ii) MOLECULE TYPE: peptide

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 T0290-2E6800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Gly Pro Val Ala Phe Asp Ser Glu Thr Ser Ala  
1 5 10

(2) INFORMATION FOR SEQ ID NO:21:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 10 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Ile Val Ser Asp Ile Glu Ala Asn Ala  
1 5 10

(2) INFORMATION FOR SEQ ID NO:22:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 26 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

20 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GACGTTTCAA GCGCTAGGGC AAAAGA

26

(2) INFORMATION FOR SEQ ID NO:23:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 31 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

05891333.062704  
T02290.21216850

GTATATTATA GAGTAGTTAA CCATCTTTCC A

31

## (2) INFORMATION FOR SEQ ID NO:24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Phe Leu Phe Asp Gly Thr  
1 5

## (2) INFORMATION FOR SEQ ID NO:25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Leu Leu Val Asp Gly His  
1 5

## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Ser Leu Ile Thr Gly Asp Lys Asp Met Leu  
1 5 10

## (2) INFORMATION FOR SEQ ID NO:27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Arg Ile Leu Thr Ala Asp Lys Asp Leu Tyr  
 1 5 10

## (2) INFORMATION FOR SEQ ID NO:28:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GTAGGCCAGG GCTGTGCCGG CAAAGAGAAA TAGTC

35

## (2) INFORMATION FOR SEQ ID NO:29:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GAAGCATATC CTTGGCGCCG GTTATTATGA AAATC

35

## (2) INFORMATION FOR SEQ ID NO:30:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

5 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CACCAGACGG GTACCGCCAC TGGCAGGTTG

30

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TATAGAGTAG TTAACCATCT TTCCAACCCG TTTCATTTCT TCGAACAC

48

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

25 TATAGAGTAG TTAACCATCT TTCCAACCCG TTGCATTTCT TCGAACAC

48

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TATAGAGTAG TTAACCATCT TTCCAACCCG GTTCATTTCT TCGAACAC

48

(2) INFORMATION FOR SEQ ID NO:34:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 48 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

10 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TATAGAGTAG TTAACCATCT TTCCAACCCG ATGCATTTCT TCGAACAC

48

(2) INFORMATION FOR SEQ ID NO:35:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 29 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AAGATGGTTA ACGCGTCTAT AATATACGG

29

(2) INFORMATION FOR SEQ ID NO:36:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 23 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

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 10/29/2006 15:58:50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CAAGAGGCAC AGAGAGTTTC ACC

23

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GTATATTATA GAGGAGTTAA CCATCTTTCC

30

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

20 AAGATGGTTA ACTTCTCTAT AATATACGG

29

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 48 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TATAGAGTAG TTAACCATCT TTCCAACCCG GTACATGTCT TCGTTCAC

48

## (2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 48 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TATAGAGTAG TTAACCATCT TTCCAACCCG CAACATGTCT TCGTTCAC

48

## (2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CTTGGCCGCC CGATGCATCA GGGGGTC

27

## (2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CTTGGCCGCC CGCTTCATGA GGGGGTCCAC

30

## (2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 base pairs



- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTTGCCCGCC CTGTACATCA GGGGGTC

27

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

15 GTATATTATA GAGGTGTTAA CCATCTTTCC

30

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GGGAGACCGG AATTCTCCTT CATTAATTCC TATA

34

25 (2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 49 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

30

T07290"2E15850

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TGGAGACCCT GGAACATATAG GAATTAATGA AGGAGAATTC CGGTCTCCC

49

(2) INFORMATION FOR SEQ ID NO:47:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

10 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GTATTTTGGT ATGCTTGTGC

20

(2) INFORMATION FOR SEQ ID NO:48:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CTATTTTGGGA ATATATGTGC CT

22

(2) INFORMATION FOR SEQ ID NO:49:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

T02290"2EET6860

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(2) INFORMATION FOR SEQ ID NO:50:

5

(ii) MOLECULE TYPE: cDNA

10

20

(2) INFORMATION FOR SEQ ID NO:51:

15

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

21

(2) INFORMATION FOR SEQ ID NO:52:

25

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

20

## (2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

AGCTTGAGAC CTCTGTGTCC

20

## 10 (2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ATTGAGAAGA AACAGTGATG GT

22

## (2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TTGGAGTCGC AAGCTGAACT AGC

23

## (2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs

(ii) MOLECULE TYPE: cDNA

23

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24

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24

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(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ACTCATGAAG GTGACAGTTC

20

(2) INFORMATION FOR SEQ ID NO:60:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

10 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GTGTTGTTGA CCTATTGCAT

20

(2) INFORMATION FOR SEQ ID NO:61:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ATCTCTGTTC CCTCCCTGTT

20

(2) INFORMATION FOR SEQ ID NO:62:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CTTATTGGCC TTGAAGGTAG

20

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

AGCCCGTGTT GGAACCATGA CTG

23

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

20 TACATAGCGA GACTCCATCT CCC

23

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TTTATGCGAG CGTATGGATA

20

000133-05701  
T0290"2226880

## (2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

CACCACCATT GATCTGGAAG

20

## 10 (2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CCAACCACAC TGGGAA

16

## (2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

AACAGTTGCC CACGGT

16

## (2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs



- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CATGAAATGC TGACTGGGTA

20

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

15 TCAATTTATG TGCAGCCAAT

20

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CATAGCGAGA CTCCATCTCC

20

25 (2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

30

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(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GGGAGAGGGC AAAGATCGAT

20

(2) INFORMATION FOR SEQ ID NO:73:

5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

10 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

AACACTAGTG ACATTATTTT CA

22

(2) INFORMATION FOR SEQ ID NO:74:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

AGCTAGGCCT GAAGGCTTCT

20

(2) INFORMATION FOR SEQ ID NO:75:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CCCTAGTGGA TGATAAGAAT AATC

24

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GGACAGATGA TAAATACATA GGATGGATGG

30

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

TTCTCTTACA AACTGCCCC

20

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

ATTTGGATGG CTTGACAGAG

20

09891330 062701

## (2) INFORMATION FOR SEQ ID NO:79:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

ACATTCTAAG ACTTTCCCAA T

21

## 10 (2) INFORMATION FOR SEQ ID NO:80:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

AGAGCATGCA CCCTGAATTG

20

## (2) INFORMATION FOR SEQ ID NO:81:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

AAGAACCATG CGATACGACT

20

## (2) INFORMATION FOR SEQ ID NO:82:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CATTCCTAGA TGGGTAAAGC

20

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

15 GCTTAGTCAT ACGAGCGG

18

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

TCCACAGCCA TGTAACC

18

25 (2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

30

09091332 062701

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

CCCCGGAGCA AGTTCA

16

(2) INFORMATION FOR SEQ ID NO:86:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 18 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

10 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

CAGCCCAAAG CCAGATTA

18

(2) INFORMATION FOR SEQ ID NO:87:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

ATATGTGAGT CAATTCCCCA AG

22

(2) INFORMATION FOR SEQ ID NO:88:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

TGTATTAGTC AATGTTCTCC AG

22

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

CAGCTGCCCT AGTCAGCAC

19

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

20 GCTTCCGAGT GCAGGTCACA

20

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

ATTCTGGGCG CACAAGAGTG A

21

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T02290-22ET880

## (2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ACATCTCCCC TACCGCTATA

20

## 10 (2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GAAGTTCACC ATCCGGCCGA CCCGTCGCAT TTC

33

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